



028723-385.ST25

SEQUENCE LISTING

<110> Tobin, Allan J.  
Erlander, Mark G.  
Kaufman, Daniel L.

<120> Cloned Glumatic Acid Decarboxylase

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<140> US 10/641,149

<141> 2003-08-15

<150> US 07/586,536

<151> 1990-09-12

<160> 8

<170> FastSEQ for Windows Version 4.0

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<212> PRT

<213> Felis

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<212> PRT

<213> Mus musculus

<400> 2

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<213> Mus musculus

<400> 3

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&lt;210&gt; 4

&lt;211&gt; 1758

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1758)

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Ala Gln Lys Phe Thr Gly Gly Ile Gly Asn Lys Leu Cys Ala Leu Leu
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ctg ctg cca gcc tgt gaa gga gaa agg ccc act ctc gca ttt ctg caa	336
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gat gta atg aac att ttg ctt cag tac gtg gtg aaa agt ttt gat aga	384
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atc tca aac cct gca gca act cac caa gac att gac ttc ctc att gaa 1728
Ile Ser Asn Pro Ala Ala Thr His Gln Asp Ile Asp Phe Leu Ile Glu
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gaa atc gaa cgc ctg gga caa gat ttg taa 1758
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<211> 585
<212> PRT
<213> Mus musculus

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Arg Ala Ala Thr Arg Lys Val Ala Cys Thr Cys Asp Gln Lys Pro Cys
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Ser Cys Pro Lys Gly Asp Val Asn Tyr Ala Leu Leu His Ala Thr Asp
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115     120     125
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Thr His Cys Gln Thr Leu Lys Tyr Ala Ile Lys Thr Gly His Pro
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195     200     205
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Gly Gly Leu Leu Met Ser	Arg Lys His Lys Trp	Lys Leu Asn Gly Val
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Gly Lys Pro Gln His Thr	Asn Val Cys Phe Trp	Phe Val Pro Pro Ser
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&lt;210&gt; 7

&lt;211&gt; 1758

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1758)

&lt;400&gt; 7

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Ser Gly Asp Ser Glu Asn Pro Gly Thr Ala Arg Ala Trp Cys Gln Val
20 25 30

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Ala Gln Lys Phe Thr Gly Gly Ile Gly Asn Lys Leu Cys Ala Leu Leu
35 40 45

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50 55 60

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Arg Ala Ala Ala Arg Lys Ala Ala Cys Ala Cys Asp Gln Lys Pro Cys
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agc tgc tcc aaa gtg gat gtc aac tac gcg ttt ctc cat gca aca gac 288
Ser Cys Ser Lys Val Asp Val Asn Tyr Ala Phe Leu His Ala Thr Asp
85 90 95

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210						215						220								
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Pro	Gly	Gly	Ala	Ile	Ser	Asn	Met	Tyr	Ala	Met	Met	Ile	Ala	Arg	Phe					
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			260						265						270					
ctc	att	gcc	ttc	acg	tct	gaa	cat	agt	cat	ttt	tct	ctc	aag	aag	gga	864				
Leu	Ile	Ala	Phe	Thr	Ser	Glu	His	Ser	His	Phe	Ser	Leu	Lys	Lys	Gly					
			275						280						285					
gct	gca	gcc	tta	ggg	att	gga	aca	gac	agc	gtg	att	ctg	att	aaa	tgt	912				
Ala	Ala	Ala	Leu	Gly	Ile	Gly	Thr	Asp	Ser	Val	Ile	Leu	Ile	Lys	Cys					
290						295						300								
gat	gag	aga	ggg	aaa	atg	att	cca	tct	gat	cct	gaa	aga	agg	att	ctt	960				
Asp	Glu	Arg	Gly	Lys	Met	Ile	Pro	Ser	Asp	Pro	Glu	Arg	Arg	Ile	Leu					
305						310						315			320					
gaa	gcc	aaa	cag	aaa	ggg	ttt	gtt	cct	ttc	ctc	gtg	agt	gcc	aca	gct	1008				
Glu	Ala	Lys	Gln	Lys	Gly	Phe	Val	Pro	Phe	Leu	Val	Ser	Ala	Thr	Ala					
			325						330						335					
gga	acc	acc	gtg	tac	gga	gca	ttt	gac	ccc	ctc	tta	gct	gtc	gct	gac	1056				



Gly Thr Thr Val Tyr Gly Ala Phe Asp Pro Leu Leu Ala Val Ala Asp	
340 345 350	
att tgc aaa aag tat aag atc tgg atg cat gtg gat gca gct tgg ggt	1104
Ile Cys Lys Lys Tyr Lys Ile Trp Met His Val Asp Ala Ala Trp Gly	
355 360 365	
ggg gga tta ctg atg tcc cga aaa cac aag tgg aaa ctg agt ggc gtg	1152
Gly Gly Leu Leu Met Ser Arg Lys His Lys Trp Lys Leu Ser Gly Val	
370 375 380	
gag agg gcc aac tct gtg acg tgg aat cca cac aag atg atg gga gtc	1200
Glu Arg Ala Asn Ser Val Thr Trp Asn Pro His Lys Met Met Gly Val	
385 390 395 400	
cct ttg cag tgc tct gct ctc ctg gtt aga gaa gag gga ttg atg cag	1248
Pro Leu Gln Cys Ser Ala Leu Leu Val Arg Glu Glu Gly Leu Met Gln	
405 410 415	
aat tgc aac caa atg cat gcc tcc tac ctc ttt cag caa gat aaa cat	1296
Asn Cys Asn Gln Met His Ala Ser Tyr Leu Phe Gln Gln Asp Lys His	
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tat gac ctg tcc tat gac act gga gac aag gcc tta cag tgc gga cgc	1344
Tyr Asp Leu Ser Tyr Asp Thr Gly Asp Lys Ala Leu Gln Cys Gly Arg	
435 440 445	
cac gtt gat gtt ttt aaa cta tgg ctg atg tgg agg gca aag ggg act	1392
His Val Asp Val Phe Lys Leu Trp Leu Met Trp Arg Ala Lys Gly Thr	
450 455 460	
acc ggg ttt gaa gcg cat gtt gat aaa tgt ttg gag ttg gca gag tat	1440
Thr Gly Phe Glu Ala His Val Asp Lys Cys Leu Glu Leu Ala Glu Tyr	
465 470 475 480	
tta tac aac atc ata aaa aac cga gaa gga tat gag atg gtg ttt gat	1488
Leu Tyr Asn Ile Ile Lys Asn Arg Glu Gly Tyr Glu Met Val Phe Asp	
485 490 495	
ggg aag cct cag cac aca aat gtc tgc ttc tgg tac att cct cca agc	1536
Gly Lys Pro Gln His Thr Asn Val Cys Phe Trp Tyr Ile Pro Pro Ser	
500 505 510	
ttg cgt act ctg gaa gac aat gaa gag aga atg agt cgc ctc tcg aag	1584
Leu Arg Thr Leu Glu Asp Asn Glu Glu Arg Met Ser Arg Leu Ser Lys	
515 520 525	
gtg gct cca gtg att aaa gcc aga atg atg gag tat gga acc aca atg	1632
Val Ala Pro Val Ile Lys Ala Arg Met Met Glu Tyr Gly Thr Thr Met	
530 535 540	
gtc agc tac caa ccc ttg gga gac aag gtc aat ttc ttc cgc atg gtc	1680
Val Ser Tyr Gln Pro Leu Gly Asp Lys Val Asn Phe Phe Arg Met Val	
545 550 555 560	
atc tca aac cca gcg gca act cac caa gac att gac ttc ctg att gaa	1728
Ile Ser Asn Pro Ala Ala Thr His Gln Asp Ile Asp Phe Leu Ile Glu	
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gaa ata gaa cgc ctt gga caa gat tta taa  
 Glu Ile Glu Arg Leu Gly Gln Asp Leu \*  
 580 585

1758

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 Ser Gly Asp Ser Glu Asn Pro Gly Thr Ala Arg Ala Trp Cys Gln Val  
 20 25 30  
 Ala Gln Lys Phe Thr Gly Gly Ile Gly Asn Lys Leu Cys Ala Leu Leu  
 35 40 45  
 Tyr Gly Asp Ala Glu Lys Pro Ala Glu Ser Gly Gly Ser Gln Pro Pro  
 50 55 60  
 Arg Ala Ala Ala Arg Lys Ala Ala Cys Ala Cys Asp Gln Lys Pro Cys  
 65 70 75 80  
 Ser Cys Ser Lys Val Asp Val Asn Tyr Ala Phe Leu His Ala Thr Asp  
 85 90 95  
 Leu Leu Pro Ala Cys Asp Gly Glu Arg Pro Thr Leu Ala Phe Leu Gln  
 100 105 110  
 Asp Val Met Asn Ile Leu Leu Gln Tyr Val Val Lys Ser Phe Asp Arg  
 115 120 125  
 Ser Thr Lys Val Ile Asp Phe His Tyr Pro Asn Glu Leu Leu Gln Glu  
 130 135 140  
 Tyr Asn Trp Glu Leu Ala Asp Gln Pro Gln Asn Leu Glu Glu Ile Leu  
 145 150 155 160  
 Met His Cys Gln Thr Thr Leu Lys Tyr Ala Ile Lys Thr Gly His Pro  
 165 170 175  
 Arg Tyr Phe Asn Gln Leu Ser Thr Gly Leu Asp Met Val Gly Leu Ala  
 180 185 190  
 Ala Asp Trp Leu Thr Ser Thr Ala Asn Thr Asn Met Phe Thr Tyr Glu  
 195 200 205  
 Ile Ala Pro Val Phe Val Leu Glu Tyr Val Thr Leu Lys Lys Met  
 210 215 220  
 Arg Glu Ile Ile Gly Trp Pro Gly Gly Ser Gly Asp Gly Ile Phe Ser  
 225 230 235 240  
 Pro Gly Gly Ala Ile Ser Asn Met Tyr Ala Met Met Ile Ala Arg Phe  
 245 250 255  
 Lys Met Phe Pro Glu Val Lys Glu Lys Gly Met Ala Ala Leu Pro Arg  
 260 265 270  
 Leu Ile Ala Phe Thr Ser Glu His Ser His Phe Ser Leu Lys Lys Gly  
 275 280 285  
 Ala Ala Ala Leu Gly Ile Gly Thr Asp Ser Val Ile Leu Ile Lys Cys  
 290 295 300  
 Asp Glu Arg Gly Lys Met Ile Pro Ser Asp Pro Glu Arg Arg Ile Leu  
 305 310 315 320  
 Glu Ala Lys Gln Lys Gly Phe Val Pro Phe Leu Val Ser Ala Thr Ala  
 325 330 335  
 Gly Thr Thr Val Tyr Gly Ala Phe Asp Pro Leu Leu Ala Val Ala Asp  
 340 345 350  
 Ile Cys Lys Lys Tyr Lys Ile Trp Met His Val Asp Ala Ala Trp Gly  
 355 360 365  
 Gly Gly Leu Leu Met Ser Arg Lys His Lys Trp Lys Leu Ser Gly Val  
 370 375 380

Glu	Arg	Ala	Asn	Ser	Val	Thr	Trp	Asn	Pro	His	Lys	Met	Met	Gly	Val	385	390	395	400
Pro	Leu	Gln	Cys	Ser	Ala	Leu	Leu	Val	Arg	Glu	Glu	Gly	Leu	Met	Gln	405	410	415	
Asn	Cys	Asn	Gln	Met	His	Ala	Ser	Tyr	Leu	Phe	Gln	Gln	Asp	Lys	His	420	425	430	
Tyr	Asp	Leu	Ser	Tyr	Asp	Thr	Gly	Asp	Lys	Ala	Leu	Gln	Cys	Gly	Arg	435	440	445	
His	Val	Asp	Val	Phe	Lys	Leu	Trp	Leu	Met	Trp	Arg	Ala	Lys	Gly	Thr	450	455	460	
Thr	Gly	Phe	Glu	Ala	His	Val	Asp	Lys	Cys	Leu	Glu	Leu	Ala	Glu	Tyr	465	470	475	480
Leu	Tyr	Asn	Ile	Ile	Lys	Asn	Arg	Glu	Gly	Tyr	Glu	Met	Val	Phe	Asp	485	490	495	
Gly	Lys	Pro	Gln	His	Thr	Asn	Val	Cys	Phe	Trp	Tyr	Ile	Pro	Pro	Ser	500	505	510	
Leu	Arg	Thr	Leu	Glu	Asp	Asn	Glu	Glu	Arg	Met	Ser	Arg	Leu	Ser	Lys	515	520	525	
Val	Ala	Pro	Val	Ile	Lys	Ala	Arg	Met	Met	Glu	Tyr	Gly	Thr	Thr	Met	530	535	540	
Val	Ser	Tyr	Gln	Pro	Leu	Gly	Asp	Lys	Val	Asn	Phe	Phe	Arg	Met	Val	545	550	555	560
Ile	Ser	Asn	Pro	Ala	Ala	Thr	His	Gln	Asp	Ile	Asp	Phe	Leu	Ile	Glu	565	570	575	
Glu	Ile	Glu	Arg	Leu	Gly	Gln	Asp	Leu								580	585		